

QY 3721 CAGCCAAAGCAGCTGAGAGAAATGCCAGTCGCCCTATGTTATTTCAGGAATCAAAGTCTT 3780
DB 3721 CAGCCAAAGCAGCTGAGAGAAATGCCAGTCGCCCTATGTTATTTCAGGAATCAAAGTCTT 3780
QY 3781 TGCTCAGAAATCCTTTTGAAGCCATCAGACCAGGAAGTGTCAACAGGTGAGACAGGCT 3840
DB 3781 TGCTCAGAAATCCTTTTGAAGCCATCAGACCAGGAAGTGTCAACAGGTGAGACAGGCT 3840
QY 3841 CACTGCTAAACCCAGCCCAAGCTGTGCTTCAGAAACTGCTCTCTCTGACCATTAACC 3900
DB 3841 CACTGCTAAACCCAGCCCAAGCTGTGCTTCAGAAACTGCTCTCTCTGACCATTAACC 3900
QY 3901 CCACTGCTCCTCGAAATTCAGAAACTTTGCTTTTCAATACACTTTCTCTGCAAGGCTG 3960
DB 3901 CCACTGCTCCTCGAAATTCAGAAACTTTGCTTTTCAATACACTTTCTCTGCAAGGCTG 3960
QY 3961 AGCGGGCAAAAGGAATCGTCTAAGTCTCAGAAAGATCCAGAGAAAGACTCTGACTGCTCA 4020
DB 3961 AGCGGGCAAAAGGAATCGTCTAAGTCTCAGAAAGATCCAGAGAAAGACTCTGACTGCTCA 4020
QY 4021 CCTGGAGTGGAGCTCCTATCCCTGGATTCTTCAGGCTTTTCAATTGACCCACATGTTAG 4080
DB 4021 CCTGGAGTGGAGCTCCTATCCCTGGATTCTTCAGGCTTTTCAATTGACCCACATGTTAG 4080
QY 4081 CTGGGAGAGACAGAGTCCAAAGAGAGGGGAGAAAGGCTATTCTGGGAGAAACAAT 4140
DB 4081 CTGGGAGAGACAGAGTCCAAAGAGAGGGGAGAAAGGCTATTCTGGGAGAAACAAT 4140
QY 4141 TGATGACTTTATGCTCTGTGTCTGTGGGAGAACTGCAATTAACCTAGATCAACCAAGCTG 4200
DB 4141 TGATGACTTTATGCTCTGTGTCTGTGGGAGAACTGCAATTAACCTAGATCAACCAAGCTG 4200
QY 4201 AGAGCCTTTAGAGTGAAGATTGGGCGGGGCGCATGCTGCTCACGCCCTGTAATCCACGA 4260
DB 4201 AGAGCCTTTAGAGTGAAGATTGGGCGGGGCGCATGCTGCTCACGCCCTGTAATCCACGA 4260
QY 4261 CTTGGGAGGCGGAGTGGGTGATGATCAAGGTCAAGAGATCAAGACCACTGACCAAC 4320
DB 4261 CTTGGGAGGCGGAGTGGGTGATGATCAAGGTCAAGAGATCAAGACCACTGACCAAC 4320
QY 4321 ATGCTGAGGCGCCCATCTCTACTAAATAATCAAAAATTAAGTGAAGTGAATGACACTG 4380
DB 4321 ATGCTGAGGCGCCCATCTCTACTAAATAATCAAAAATTAAGTGAAGTGAATGACACTG 4380
QY 4381 TAAATCCAGCTACTCGGGAGGCTGAGGCGGGGAGAAATCGCTTGAACCCGGGAGTTGAGG 4440
DB 4381 TAAATCCAGCTACTCGGGAGGCTGAGGCGGGGAGAAATCGCTTGAACCCGGGAGTTGAGG 4440
QY 4441 TTGGGTTGGGCGGAGATTGGCCCACTGCACTCCAGCCTGGGCGACAGAGCGGACTCCAT 4500
DB 4441 TTGGGTTGGGCGGAGATTGGCCCACTGCACTCCAGCCTGGGCGACAGAGCGGACTCCAT 4500
QY 4501 CTCAAAAAAGTGAAGATTGGGTCAACCCAGGCTGAAGGCCAGGGGAA 4560
DB 4501 CTCAAAAAAGTGAAGATTGGGTCAACCCAGGCTGAAGGCCAGGGGAA 4560
QY 4561 CCTGAATGATAAGGAGGAGAAACTAGGCCACAGTCTGATTGAATAAGGGGCTGAATT 4620
DB 4561 CCTGAATGATAAGGAGGAGAAACTAGGCCACAGTCTGATTGAATAAGGGGCTGAATT 4620
QY 4621 CCACCCCTGTTTCTTACTGAGAGATCAATTGAATTAAGTCTGCTCTCTCTTATTTC 4680
DB 4621 CCACCCCTGTTTCTTACTGAGAGATCAATTGAATTAAGTCTGCTCTCTCTTATTTC 4680
QY 4681 CTTTTCCTTTTAAATAGTCATCAATAATAAATTTCTTTCCAAAAA 4740
DB 4681 CTTTTCCTTTTAAATAGTCATCAATAATAAATTTCTTTCCAAAAA 4739
QY 4741 AAAAAA 4756
DB 4740 AAAAAA 4755

RESULT 2
ABV30199
ID ABV30199 standard; cDNA; 4804 BP.
XX
AC ABV30199;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 30190.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
PN WO200160860-A2.
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
PI WPI; 2001-662795/76.
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 6542-6543; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 4804 BP; 1605 A; 910 C; 1244 G; 1016 T; 29 other;
XX
Query Match 99.3%; Score 4723.8; DB 23; Length 4804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4725; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GACGGCGGAGCGCGTCTCTCCGGCTGAGGGAATCAGACAGACTCCGCTCCTAGTGA 60
DB 49 GACGGCGGAGCGCGTCTCTCCGGCTGAGGGAATCAGACAGACTCCGCTCCTAGTGA 108
QY 61 GCGCAGGGAGGCGCAGAGTATGACAGCGCAGAGTGGGTCTGAGGTTCACTCAGAAATCA 120
DB 109 GCGCAGGGAGGCGCAGAGTATGACAGCGCAGAGTGGGTCTGAGGTTCACTCAGAAATCA 168
QY 121 ATGACCCAAACGTATTTCACAGAGAGAAAGCATAGTCTTTCAGATAGTGGACAGGGCA 180

Db 169 ATGACCCAAACGTCATTTTCACAAGAGGAGCAGATAGTCCTTCAGATAGTGGACAGGCA 228
 QY 181 GCTATGAAACAAATTGGACCCCTTGAGTGAAGAGATTCAGATGAAGAGATATTGTAAGTA 240
 Db 229 GCTATGAAACAAATTGGACCCCTTGAGTGAAGAGATTCAGATGAAGAGATATTGTAAGTA 288
 QY 241 AGAAGTGAAGAAACAGGAGAGTCTTCAAGACAGTGTCCGAAACAGAGGACACAAATG 300
 Db 289 AGAAGTGAAGAAACAGGAGAGTCTTCAAGACAGTGTCCGAAACAGAGGACACAAATG 348
 QY 301 CCTCTCCAGAGAAACTACCTATGACAGTGGCCGAGAGGAAATTAAGAGATTTATATG 360
 Db 349 CCTCTCCAGAGAAACTACCTATGACAGTGGCCGAGAGGAAATTAAGAGATTTATATG 408
 QY 361 CTGGGAAAAATACAAAAATCAAAAGATTACAAAACCTGTGGCAGACAGTGAAGTT 420
 Db 409 CTGGGAAAAATACAAAAATCAAAAGATTACAAAACCTGTGGCAGACAGTGAAGTT 468
 QY 421 ACATGAAAAAGTCTTTGTATCAGGAAATCTTGAAGCGCAAGTGAACCTTGTAGAGC 480
 Db 469 ACATGAAAAAGTCTTTGTATCAGGAAATCTTGAAGCGCAAGTGAACCTTGTAGAGC 528
 QY 481 TGAGTCTCAGTCTGGAAACCTTACAGACTTTACCACTGACAGAAAGAGTTCCAAAAGC 540
 Db 529 TGAGTCTCAGTCTGGAAACCTTACAGACTTTACCACTGACAGAAAGAGTTCCAAAAGC 588
 QY 541 ACATACATGATTAAGAGAGAACTGCAAGAAAGCAAAAGTAAATCAAAAAGAGAGCTTG 600
 Db 589 ACATACATGATTAAGAGAGAACTGCAAGAAAGCAAAAGTAAATCAAAAAGAGAGCTTG 648
 QY 601 AGAAAG 660
 Db 649 AGAAAG 708
 QY 661 AGGAAGATGATGTAAGACAGCCATTTAATGACAGTGGCTGTCTTCTGTGATTAAGACC 720
 Db 709 AGGAAGATGATGTAAGACAGCCATTTAATGACAGTGGCTGTCTTCTGTGATTAAGACC 768
 QY 721 TTTTGAACCTGGGTGGAGATGAATAAATACTCTCCATTTGGAAGTGAAGATCATAG 780
 Db 769 TTTTGAACCTGGGTGGAGATGAATAAATACTCTCCATTTGGAAGTGAAGATCATAG 828
 QY 781 AATCAATAG 840
 Db 829 AATCAATAG 888
 QY 841 TGGAGAGTGGGTCATTCATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 889 TGGAGAGTGGGTCATTCATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 948
 QY 901 AGGAAG 960
 Db 949 AGGAAG 1008
 QY 961 AGGCGCTTATTCGAGAGTCTGACAGTGAACCTTCCATATCATATGCTGAGATTAAGACA 1020
 Db 1009 AGGCGCTTATTCGAGAGTCTGACAGTGAACCTTCCATATCATATGCTGAGATTAAGACA 1068
 QY 1021 TGCATGATTTCTCAACGTAACCCCGGCGCCACTTGCACAGGAATGCCATGGCAGCTAT 1080
 Db 1069 TGCATGATTTCTCAACGTAACCCCGGCGCCACTTGCACAGGAATGCCATGGCAGCTAT 1128
 QY 1081 TGAAGTCACTTAATATCAGTCAAGCCATCACAAGAAATCATAGACACTGCAATACTA 1140
 Db 1129 TGAAGTCACTTAATATCAGTCAAGCCATCACAAGAAATCATAGACACTGCAATACTA 1188
 QY 1141 CTGAATAGACAGTGTATCAGTCAAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 Db 1189 CTGAATAGACAGTGTATCAGTCAAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1248
 QY 1201 AAGTGAAG 1260
 Db 1249 AAGTGAAG 1308

QY 1261 ATGAGTCTTGCAGAGAGAGATTTGGTAATAAATGAAGAGCTAGAAATTCAGAGAGAGAGAG 1320
 Db 1309 ATGAGTCTTGCAGAGAGAGATTTGGTAATAAATGAAGAGCTAGAAATTCAGAGAGAGAGAG 1368
 QY 1321 AGCAGAGTGAATAGACCTTCACCTGGGGACAGCTCAGTGTGCAACAGGAATCCAACT 1380
 Db 1369 AGCAGAGTGAATAGACCTTCACCTGGGGACAGCTCAGTGTGCAACAGGAATCCAACT 1428
 QY 1381 TCCCTGGGGAACAATACAGTGAAGAGATGTCAGGTTGAGAGGCTTGTAGCATTTGAACCTC 1440
 Db 1429 TCCCTGGGGAACAATACAGTGAAGAGATGTCAGGTTGAGAGGCTTGTAGCATTTGAACCTC 1488
 QY 1441 ATGCCCCGAGAGGAG 1500
 Db 1489 ATGCCCCGAGAGGAG 1548
 QY 1501 CTGAGCAGCAAAATTAATCATCAGCAGTGGGCGCCACCTGAAAAAGTGAGACGGTTACTC 1560
 Db 1549 CTGAGCAGCAAAATTAATCATCAGCAGTGGGCGCCACCTGAAAAAGTGAGACGGTTACTC 1608
 QY 1561 TGGATGACCTTAAGCACTGGGAGTGAATGTTCCATTAAACCAAGGCTAGGTGCTGATG 1620
 Db 1609 TGGATGACCTTAAGCACTGGGAGTGAATGTTCCATTAAACCAAGGCTAGGTGCTGATG 1668
 QY 1621 AAGATTCCTTTGTGATCTTGAACCTGAAACCAACAGAGAGAGAGAGAGAGAGAGAGAG 1680
 Db 1669 AAGATTCCTTTGTGATCTTGAACCTGAAACCAACAGAGAGAGAGAGAGAGAGAGAGAG 1728
 QY 1681 GTTCTGGAAGCATGCTAATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 Db 1729 GTTCTGGAAGCATGCTAATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1788
 QY 1741 AGCTCATAGTGAAG 1800
 Db 1789 AGCTCATAGTGAAG 1848
 QY 1801 CTGTGACTTTAGCAGCTTAAG 1860
 Db 1849 CTGTGACTTTAGCAGCTTAAG 1908
 QY 1861 TTCAGTGTAAAAAGCTAACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
 Db 1909 TTCAGTGTAAAAAGCTAACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1968
 QY 1921 AGAAGCGCAAGCAGCTGTTAAATTAATTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
 Db 1969 AGAAGCGCAAGCAGCTGTTAAATTAATTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2028
 QY 1981 AAG 2040
 Db 2029 AAG 2088
 QY 2041 AGAAG 2100
 Db 2089 AGAAG 2148
 QY 2101 ATCAG 2160
 Db 2149 ATCAG 2208
 QY 2161 AATGAG 2220
 Db 2209 AATGAG 2268
 QY 2221 CTGTTCCAGAGTCTCTCATCAGATTCATCTTACTTCTGTTTAAAGAGAGAGAGAGAGAGAG 2280
 Db 2269 CTGTTCCAGAGTCTCTCATCAGATTCATCTTACTTCTGTTTAAAGAGAGAGAGAGAGAGAG 2328
 QY 2281 AGATGGGTTACTCTCTCATCAGATTCATCTTACTTCTGTTTAAAGAGAGAGAGAGAGAGAG 2340
 Db 2329 AGATGGGTTACTCTCTCATCAGATTCATCTTACTTCTGTTTAAAGAGAGAGAGAGAGAGAG 2388

| | | | |
|----|------|--|------|
| QY | 2341 | CTAGCAAACTGGATGAGATGATTCATCTGTTCAATTTGCTATAACAAGAGAGAGACGCCACATA | 2400 |
| Db | 2389 | CTAGCAAACTGGATGAGATGATTCATCTGTTCAATTTGCTATAACAAGAGAGAGACGCCACATA | 2448 |
| QY | 2401 | GCAGCTTTGAGCTGATTGGCTCCACAGATTCCATCCTATCAGCCTTGCAACAGACAACAG | 2460 |
| Db | 2449 | GCAGCTTTGAGCTGATTGGCTCCACAGATTCCATCCTATCAGCCTTGCAACAGACAACAG | 2508 |
| QY | 2461 | GCCGTGGGAACCAAGTTTTCCTCCACAGCAGAGGAGATTTCAGATCTTCCTTCCCTGGGCTAT | 2520 |
| Db | 2509 | GCCGTGGGAACCAAGTTTTCCTCCACAGCAGAGGAGATTTCAGATCTTCCTTCCCTGGGCTAT | 2568 |
| QY | 2521 | TTCCAGCCAGTTTGGTCACTCAGCTTCTAAGAGTTTCAGGGAACCTGTCTGAGCCTTCAC | 2580 |
| Db | 2569 | TTCCAGCCAGTTTGGTCACTCAGCTTCTAAGAGTTTCAGGGAACCTGTCTGAGCCTTCAC | 2628 |
| QY | 2581 | TTCCCATAGAGGATTTCCCAAGATCTGTATTAACGCCCTCCCCAGAGCCTTAAGACACTTTCC | 2640 |
| Db | 2629 | TTCCCATAGAGGATTTCCCAAGATCTGTATTAACGCCCTCCCCAGAGCCTTAAGACACTTTCC | 2688 |
| QY | 2641 | TAGAGCAGAGAGACTTCCAGTTCTGTTAGAGATGACACTCAGAGCCCACTGTGGATG | 2700 |
| Db | 2689 | TAGAGCAGAGAGACTTCCAGTTCTGTTAGAGATGACACTCAGAGCCCACTGTGGATG | 2748 |
| QY | 2701 | CAGATGGGTTCTTAATGTTAGAAACCACAGAAATCAGTACCAGCTTTGAAGCCTCGAT | 2760 |
| Db | 2749 | CAGATGGGTTCTTAATGTTAGAAACCACAGAAATCAGTACCAGCTTTGAAGCCTCGAT | 2808 |
| QY | 2761 | TGCCATTGGCCAGTATGATGAGATGCCATGATGCCACATGATGATGAGCTGTGGATT | 2820 |
| Db | 2809 | TGCCATTGGCCAGTATGATGAGATGCCATGATGCCACATGATGATGAGCTGTGGATT | 2868 |
| QY | 2821 | TGTGTACTGAAAAGTTCAACATCTCAGGCTGAAAAACATCTACCAGAGAGAGTGACACAGA | 2880 |
| Db | 2869 | TGTGTACTGAAAAGTTCAACATCTCAGGCTGAAAAACATCTACCAGAGAGAGTGACACAGA | 2928 |
| QY | 2881 | AAGAGAACATGAGGAACCTTCTGAACCTTTGTTCAAGAAAAATTCATCTCAGAGATGGCT | 2940 |
| Db | 2929 | AAGAGAACATGAGGAACCTTCTGAACCTTTGTTCAAGAAAAATTCATCTCAGAGATGGCT | 2988 |
| QY | 2941 | CCACTCCAGCCTCATCAGAGTTAAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 3000 |
| Db | 2989 | CCACTCCAGCCTCATCAGAGTTAAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 3048 |
| QY | 3001 | TGGAAGAAGCACTTGCTCTTTGCTCAGGCTCTTTTCCACAGACAAAGAAAGAAAGAGAG | 3060 |
| Db | 3049 | TGGAAGAAGCACTTGCTCTTTGCTCAGGCTCTTTTCCACAGACAAAGAAAGAAAGAGAG | 3108 |
| QY | 3061 | AGGAGAGAGAAATTTGGAGACTTTCGGCTTGTTCATAATGATTAATGAGTTTGATAGTAGG | 3120 |
| Db | 3109 | AGGAGAGAGAAATTTGGAGACTTTCGGCTTGTTCATAATGATTAATGAGTTTGATAGTAGG | 3168 |
| QY | 3121 | AGGATGAACACAGTGAAGTCTGGTAAATGATCTGGCACTGGAAGAACCATGAAGATGATGATG | 3180 |
| Db | 3169 | AGGATGAACACAGTGAAGTCTGGTAAATGATCTGGCACTGGAAGAACCATGAAGATGATGATG | 3228 |
| QY | 3181 | AAGAAGAAGCTCCTGAAGCGATCTGAGAAAGTTGAAAAAGCCAAATGAGCTTGAGGAATACC | 3240 |
| Db | 3229 | AAGAAGAAGCTCCTGAAGCGATCTGAGAAAGTTGAAAAAGCCAAATGAGCTTGAGGAATACC | 3288 |
| QY | 3241 | TGGAGGATGAGGCGAGAGGTGTCAAGGAAGTGAATGTGGGAAGCGAAGATGATGATGGGG | 3300 |
| Db | 3289 | TGGAGGATGAGGCGAGAGGTGTCAAGGAAGTGAATGTGGGAAGCGAAGATGATGATGGGG | 3348 |
| QY | 3301 | AAGAATTTGATGAATATGAAGAGAGCGTAATGATGATGATGATGATGATGATGATGATGATG | 3360 |
| Db | 3349 | AAGAATTTGATGAATATGAAGAGAGCGTAATGATGATGATGATGATGATGATGATGATGATG | 3408 |
| QY | 3361 | TGCAGAGTCAAAATCAAGAAATATACATGAAAACTATGTTGGATGATGATTAAGCGACAGC | 3420 |
| Db | 3409 | TGCAGAGTCAAAATCAAGAAATATACATGAAAACTATGTTGGATGATGATTAAGCGACAGC | 3468 |
| QY | 3421 | TACGTTTATACCAAGAGAGGTACCTTCTGATGGGATCTGCACAGCGATGCTCTGGGC | 3480 |

| | | | |
|----|------|--|------|
| Db | 3469 | TACGTTTATACCAAGAGAGGTACCTTGCTGATGGGGATCTGCACAGCGATGGTCTCGGGC | 3528 |
| QY | 3481 | GAATGAGGAAGTTTCGATGGAAAAACATAGATGATGCTTCCAGATGGACTTGTTCACA | 3540 |
| Db | 3529 | GAATGAGGAAGTTTCGATGGAAAAACATAGATGATGCTTCCAGATGGACTTGTTCACA | 3588 |
| QY | 3541 | GAGACTCTGATGATGATCAGACTGAAGACAGCTTGATGAGTCAGAAAGCCAGGTGAGGA | 3600 |
| Db | 3589 | GAGACTCTGATGATGATCAGACTGAAGACAGCTTGATGAGTCAGAAAGCCAGGTGAGGA | 3648 |
| QY | 3601 | AGGAGCGAATTGAACGAGAGCAGTGGCTTCGGGACATGGCCAGCAGGGGAAATACAG | 3660 |
| Db | 3649 | AGGAGCGAATTGAACGAGAGCAGTGGCTTCGGGACATGGCCAGCAGGGGAAATACAG | 3708 |
| QY | 3661 | CTGAAGAAGAAGAATAATGGGGAGGACAGTCAGTTTATGATACTGGCCAGAAAGTTA | 3720 |
| Db | 3709 | CTGAAGAAGAAGAATAATGGGGAGGACAGTCAGTTTATGATACTGGCCAGAAAGTTA | 3768 |
| QY | 3721 | CAGCCAAAGCAGCTGCAGAGAATGCCAGTCGCCCTATGGTTATTCAGGAATCAAGTCTT | 3780 |
| Db | 3769 | CAGCCAAAGCAGCTGCAGAGAATGCCAGTCGCCCTATGGTTATTCAGGAATCAAGTCTT | 3828 |
| QY | 3781 | TGCTCAGAAATCCTTTTGAAGCCATCAGACGAGGAAGTGTCTCAACAGGTGAAGACAGCT | 3840 |
| Db | 3829 | TGCTCAGAAATCCTTTTGAAGCCATCAGACGAGGAAGTGTCTCAACAGGTGAAGACAGCT | 3888 |
| QY | 3841 | CAGTCCTAAACGAGCCCAAGAGCTGTGCTTCAGAAACTGGCTGCTCTCTCTGACCATTAAC | 3900 |
| Db | 3889 | CAGTCCTAAACGAGCCCAAGAGCTGTGCTTCAGAAACTGGCTGCTCTCTCTGACCATTAAC | 3948 |
| QY | 3901 | CCAGTGTCTCTCGAAATTCAGAAACTTTGTCTTTCATACACTTCTCTCTGCAAGGCTG | 3960 |
| Db | 3949 | CCAGTGTCTCTCGAAATTCAGAAACTTTGTCTTTCATACACTTCTCTCTGCAAGGCTG | 4008 |
| QY | 3961 | AGGCGGCAAGGAATCGTCTAAGTCTCAGAGAATCCGAGAGAAGGACTCTGACTGGCTCA | 4020 |
| Db | 4009 | AGGCGGCAAGGAATCGTCTAAGTCTCAGAGAATCCGAGAGAAGGACTCTGACTGGCTCA | 4068 |
| QY | 4021 | CCTGGAGTGGAGCTCCCTATCCCTGGATTCTTAAAGCCTTTCATTTGACCCACATGTTAA | 4080 |
| Db | 4069 | CCTGGAGTGGAGCTCCCTATCCCTGGATTCTTAAAGCCTTTCATTTGACCCACATGTTAA | 4128 |
| QY | 4081 | CTGGGAGACACAGAGTCCCAAGAGAGCGGAGAGAGGGCTATTCTGGGACAGAACAAACAAT | 4140 |
| Db | 4129 | CTGGGAGACACAGAGTCCCAAGAGAGCGGAGAGAGGGCTATTCTGGGACAGAACAAACAAT | 4188 |
| QY | 4141 | TGATGACTTTATGGCTCTGTGGTCTGGGACAGAACTGCATTAACCTTAGATCACCAGGCTG | 4200 |
| Db | 4189 | TGATGACTTTATGGCTCTGTGGTCTGGGACAGAACTGCATTAACCTTAGATCACCAGGCTG | 4248 |
| QY | 4201 | AGAGCCTTTAGGAGTGAAGATTGGGGCCGGGCAATGGTGGCTCACGCGCTGTATCCACAGA | 4260 |
| Db | 4249 | AGAGCCTTTAGGAGTGAAGATTGGGGCCGGGCAATGGTGGCTCACGCGCTGTATCCACAGA | 4308 |
| QY | 4261 | CTTTGGAGGCGCGAGGTGGGTGGATCACAAAGTCAAGGATCAAGACCAACCTGACCAAC | 4320 |
| Db | 4309 | CTTTGGAGGCGCGAGGTGGGTGGATCACAAAGTCAAGGATCAAGACCAACCTGACCAAC | 4368 |
| QY | 4321 | ATGTTGAGGCGCCCATCTCTACTAAAAATACAAAAATTAGCTGACGCTGATGCATGCACCTG | 4380 |
| Db | 4369 | ATGTTGAGGCGCCCATCTCTACTAAAAATACAAAAATTAGCTGACGCTGATGCATGCACCTG | 4428 |
| QY | 4381 | TAAATCCAGCTACTCGGAGGCTGAGGCGGAGAAATCGCTGAACCCGGGAGGTTGGAGG | 4440 |
| Db | 4429 | TAAATCCAGCTACTCGGAGGCTGAGGCGGAGAAATCGCTGAACCCGGGAGGTTGGAGG | 4488 |
| QY | 4441 | TTGCGGTGGGCGGAGATTGCGCCACTGCACCTCAGCCTGGGGGACAGAGCGGACTCCAT | 4500 |
| Db | 4489 | TTGCGGTGGGCGGAGATTGCGCCACTGCACCTCAGCCTGGGGGACAGAGCGGACTCCAT | 4548 |
| QY | 4501 | CTCAAAAAAAAAAAAAAAAAAGTGAGATTGGGTCAACCCAGGCTGAAGGCCAGGGGAA | 4560 |

Db 4549 CTCAAAAAAAAAAAAAAAAAGTGAGATTGGGTACCCACAGGCTGAAGGCCAGGGGAA 4608
QY 4561 CCTGAATGATAAGGGAAGGAACTTAGGCCACAGTCTGATTAGAAATGGGGCTGAATT 4620
Db 4609 CCTGAATGATAAGGGAAGGAACTTAGGCCACAGTCTGATTAGAAATGGGGCTGAATT 4668
QY 4621 CCACCCCTGTTTTCCTTACTGGAGATTCATTGAAATTAATCTGCTCCCTCTTATTC 4680
Db 4669 CCACCCCTGTTTTCCTTACTGGAGATTCATTGAAATTAATCTGCTCCCTCTTATTC 4728
QY 4681 CTTTCCCTTTTAAATAGTCATCATATCAATAAAATTTCTTTCC 4727
Db 4729 CTTTCCCTTTTAAATAGTCATCATATCAATAAAATTTCTTTCC 4775
RESULT 3
ABK52610
ID ABK52610 standard; DNA; 4754 BP.
XX
AC ABK52610;
XX
DT 27-AUG-2002 (first entry)
XX
DE DNA encoding Xenopus Claspin protein.
XX
KW Chk1 protein; SQ/TQ motif; isoelectric point; cell cycle progression;
KW nuclear localisation signal; DNA replication checkpoint; benign neoplasm;
KW cell proliferative disorder; malignant neoplasm; frog; claspin; gene; ds.
XX
OS Xenopus sp.
XX
FH Key Location/Qualifiers
FT CDS 71..3928
FT /tag= a
FT /product= "Xenopus Claspin protein"
XX
PN WO200233115-A2.
XX
PD 25-APR-2002.
XX
PE 17-OCT-2001; 2001WO-US32316.
XX
PR 17-OCT-2000; 2000US-241246P.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Kumagai A, Dunphy WG;
XX
DR WPI; 2002-452394/48.
DR P-PSDB; AA097586.
XX
PT Novel Claspin polypeptide specifically interacting with Chk1 protein
PT useful for identifying compound that modulates cell cycle progression
PT and for treating cell proliferative disorder like neoplasm
XX
PS Claim 7; Fig 1; 97pp; English.
XX
CC The present invention relates to a new substantially pure Claspin
CC polypeptide that specifically interacts with a Chk1 protein, having SQ/TQ
CC motifs, an isoelectric point of 4.5 and at least one nuclear localisation
CC signal. The method of the invention is useful for identifying a compound
CC that modulates cell cycle progression and for modulating cell cycle
CC progression in a cell. The invention is useful for the proper operation
CC of DNA replication checkpoint in the cell cycle. The method is also
CC useful for treating a disorder associated with cell cycle progression
CC e.g. cell proliferative disorder such as benign or malignant neoplasm.
CC The molecules of the invention are also useful for detecting the altered
CC levels of claspin expression. The present nucleic acid sequence encodes
CC the Xenopus Claspin protein of the invention.
XX
SQ Sequence 4754 BP; 1658 A; 832 C; 1066 G; 1198 T; 0 other;

Query Match

15.4%; Score 730.2; DB 24; Length 4754;

Best Local Similarity 54.3%; Pred. No. 3e-111;
Matches 2085; Conservative 0; Mismatches 1523; Indels 231; Gaps 21;
QY 184 ATGAACAATATGACCCCTTGAGTGAAGAGATTGAGATGAAGATATTTGTAAGTAGA 243
Db 186 ATAAATATTTGGGTGTGTGAGAGATTAAGATACAGATGATGAATCTTGCTGTA 245
QY 244 AGTTGAAAAACAGGAAGGTTCTTACAGACAGTGA---TTCCGAAACAGAGACACAAATG 300
Db 246 AATCTAAAAAGAGAGAGATATTGGTGATAGTGACAGTGAAGAAATGGAAATGCGTA 305
QY 301 CCTCTCCAGAGAAAACTACCTATGACAGTCCCGAGGAGGAAAAATAAGAGATTATATG 360
Db 306 ATTTTGCAGATAATGTAAAGGGGCACCTCTGATTAATGAGGAAATGAGAGACTATGCTG 365
QY 361 CTGGGAAAAATACAAAAATCAAAAGGATTTACAAAACCTGTGGCAGACAGTGAAGATT 420
Db 366 CTATATAGAGA--AAACCAAGAAAGATCCGTTCAAGCTGTATTGGACAGTGAATAGTG 422
QY 421 ACATGGAAGAGTCTTTGTATCAGGAAATCTTGAAGCGCAAGTGAACCTTGCTTAGAGC 480
Db 423 ATCATGAGCTTGATGTTCAAAATAGTACAAAGTCAAAATGCAAGCTGAATACCTGAGTCAG 482
QY 481 TGAGTCTTCAGTCTGGAACCTCTACAGACTTTACCACTGACAGAAAGAGTTCCAAAAAGC 540
Db 483 AACATGATAGCTTGAGAGAAAGAACTCACTGTGAAAGCTTAAACAGCAAGTCTTGA 542
QY 541 ACATACATGATTAAGAGAACTGACAGAAAGCAAAAGTAAATCAAAAAGAGAACTTG 600
Db 543 AAAAACCAACTGACACTAATTAAGAGAAATCGTGAAGAAATTAATCAAAAGCCCAAAATTC 602
QY 601 AGAAAGAGGAGAGAAAAATGAAAAAATTGACAGCTAAAAAAGAGAAACAAAAACC 660
Db 603 CGAAGAGAGAGATTAAAGAGAGACAAACAGAAAGTCAAAAGCA----- 646
QY 661 AGAAGATGATGTAGAACAGCCATTTAATGACAGTGGCTGCTCTTGTGATAAAGACC 720
Db 647 -GTGCTGAAGCTAGGCCAAATTTAAATGACAGTGGCTGCTTACTACAGATGAGATC 704
QY 721 TTTTGAACCTGGGTGAGAGATGAATAAATTAATCTCCATTTGAAAGATGAAGATCATTAG 780
Db 705 TTTTGAACAATGGGTGAGAAATGAGATGATCT--AATGAAGAGAGAGATCTCTTG 761
QY 781 AATCAATAAGACAGCTGTAAAAAACAAGTAAAAAAGCACAAGAAAAAGAACCATCTT 840
Db 762 AAGCTATCCGGCAAAAATGAAAAAGCAACT-----GAATAGTCATCTGCTG 809
QY 841 TGGAGAGTGGGTCCATTCATTTGAGAGAGAGAGTGAATTAACAAAGAACCAAGAGA 900
Db 810 AAAATTTTGAAGACTTTGAACCTTGATACTGAAGCAATCAAGAAATCCCCAGAAAAAGAA 869
QY 901 AGAAGAGAAAGCAGCAGATTAAGTAAGAAGCATTAAGAAACAACTGCATAGTGAAGACTC 960
Db 870 AGGAAGCAAAAGCTGCGGCACTTGTAAGAACCAATGAACAAATGCACAGTGAAGACC 929
QY 961 AGCGCCTTATTCGAGAGTCTGCACCTGAACCTTCATATCATATGCTGAGAAATAAACCA 1020
Db 930 AAAGACTAATACGTGAATCTTCTGTATCTTTACCATATCATCTACCTGAACCAAAAACAA 989
QY 1021 TTCATGATTTCTTCAACAGTAACCCCGGCCCACTTGCCACGGAATGCCATGGCACTAT 1080
Db 990 TCCATGATTTTTCAAAAGCGCTCCAGAGGCTCTTTGTCAAGGAATGCAATGCACTTA 1049
QY 1081 TGAAGTCTCTAATATATAGTCAAGCCATACAAAGAAATCATAGACACTGCAATACTA 1140
Db 1050 TAAAGTCAACAAATATCACAGCCCTGCACTGAAGAGAAAAAAACCCCAATG----- 1100
QY 1141 CTGAATGAACAGTATCAACCATAGTAAGAGTTCTGAGCAGACAAACAGGTGCAGAAATG 1200
Db 1101 -----AGGAATATGTGCTGAGAGTTTC 1121
QY 1201 AAGTGAACCTAATGACATCTCCCTGTAGTTTCAAGGAAACCAAGATCATTTACTGATCAG 1260